REMARKS

Claim amendments

Claims 7, 12-14, 27, 44 and 60 have been canceled.

Claims 1, 10 and 11 have been amended to indicate that the DNA fragment obtained in the method is combined with *a DNA microarray* comprising one or more sequences complementary to one or more intergenic regions of genomic DNA of the cell, under conditions in which hybridization between the DNA fragment and the one or more sequences complementary to one or more intergenic regions of the genomic DNA occurs. Support for the amendment can be found, for example, on page 4, line 5 and page 15, line 22 of the specification.

Claims 71-86 have been added. New Claim71 is directed to a method of identifying regions across a genome of a cell where binding of DNA binding proteins occurs, comprising the steps of: a) crosslinking DNA binding proteins in the cell to genomic DNA of the cell, thereby producing DNA binding proteins crosslinked to genomic DNA; b) generating DNA fragments of the genomic DNA crosslinked to DNA binding proteins in a), thereby producing a mixture comprising DNA fragments to which DNA binding proteins are bound; c) removing DNA fragments to which the DNA binding proteins are bound from the mixture produced in b); d) separating the DNA fragments identified in c) from the DNA binding proteins; e) amplifying the DNA fragments of d); f) combining the DNA fragments of e) with DNA comprising sequences complementary to intergenic regions of genomic DNA of the cell, under conditions in which hybridization between the DNA fragments and the sequences complementary to the intergenic regions of the genomic DNA occurs; and g) identifying the sequences complementary to the intergenic regions of genomic DNA of f) to which the DNA fragments hybridize, whereby the regions identified in g) are regions across the genome of the cell where binding of DNA binding proteins occur. Support for the amendment can be found, for example, on page 11, line 11-27 of the specification.

Support for Claim 72 can be found on page 13, line 20; support for Claim 73 can be found on page 14, line 24; support for Claim 74 can be found on page 15, lines 1-2; support for Claim 75 can be found on page 15, lines 7-9; support for Claim 76 can be found on page 15, lines

5-6; support for Claims 77 and 78 can be found on page 18, lines 1-3; support for Claim 79 can be found on page 3, line 11; support for Claim 80 can be found on page 5, line 11; support for Claim 81 can be found on page 14, line 7; support for Claim 82 can be found on page 40, line 19; support for Claim 83 can be found on page 14, lines 17-18; support for Claim 84 can be found on page 5, line 16; support for Claim 85 can be found on page 13, line 4; and support for Claim 86 can be found on page 43, lines 21 -25 and page 45, line 5.

No new matter has been added.

Authorization To Act In A Representative Capacity

Applicants direct the Examiner's attention to the Authorization To Act In A Representative Capacity being filed concurrently.

Request for Change of Docket Number and Corrected Filing Receipt

Applicants direct the Examiner's attention to the Transmittal of Request for Change of Docket Number and Corrected Filing Receipt being filed concurrently.

Election/Restriction

The Examiner acknowledges "Applicant's election without traverse of Group I, claims 1-11 and 15-70 in the reply filed on January 10, 2005" (Office Action, page 2).

Applicants respectfully disagree. Applicants direct the Examiner's attention to Applicants' traversal of the restriction requirement on pages 15-16 of the reply filed January 10, 2005.

Claim interpretation

The Examiner states that the term "intergenic" includes "any region in the genome which is 'between two genes' where a gene is an open reading frame" (Office Action, page 2).

Applicants respectfully disagree with this interpretation. As would be known to one of ordinary skill in the art, an intergenic region would not include a transcribed region of a gene; however, a transcribed region of a gene can include non-coding regions, *e.g.*, such as intron sequences as well as 5' or 3' untranslated regions outside of an open reading frame.

The Examiner states that the term "microarray" is "simply any substrate with which a nucleic acid can be hybridized" (Office Action, page 2).

Applicants respectfully disagree. Applicants' claimed invention is directed to the use of a DNA microarray. As understood in the art, a "DNA microarray" is an orderly arrangement of DNA fragments, which can represent the genome of an organism, present on a surface. Each fragment is a defined sequence which is assigned a specific, discrete location on the surface. As a result, DNA microarrys can comprise numerous probes to which a nucleic acid can hybridize. In contrast, other substrates with which a nucleic acid can be hybridized, such as a Southern analysis, is a much less ordered arrangement of unknown sequences from a fragmented DNA to which a single probe can be hybridized. Therefore, a DNA microarray is a significant technological advancement in the area of substrates "with which a nucleic acid can be hybridized."

The Examiner states that the "term 'consensus DNA binding region' in claim 21 does not structurally distinguish from a particular DNA binding region and is broadly read as any DNA binding region" (Office Action, page 2).

Applicants respectfully disagree. A consensus DNA binding region is an "idealized sequence that represents the base most often present at each position" and is "defined by aligning all know examples so as to maximize their homology" (Benjamin Lewin, *Genes IV*, Oxford university Press, 1997, which is being filed herewith as the Exhibit).

Rejection of Claims 1-8, 10, 11, 17-22, 39-45, 48-53, 56-61 and 64-68 under 35 U.S.C. §102(b)

Claims 1-8, 10, 11, 17-22, 39-45, 48-53, 56-61 and 64-68 are rejected under 35 U.S.C. §102(b) "as being anticipated by Orlando et al." (Office Action, page 3). The Examiner states that Orlando *et al.* teach "a method of Claims 1, 10 and 11 for identifying a region of a genome of a cell to which a protein of interest binds" using the steps recited in Applicants' claimed method (Office Action, page 3).

Orlando *et al.* teach "a PCR and hybridization strategy that allows the identification of all binding sites of ***a particular protein*** within a genomic region of interest. According to the method of Orlando *et al.*, DNA associated with specifically immunopurified chromatin is

amplified by PCR and used ***as a probe in a Southern analysis*** of ***a given genomic region***" (Orlando *et al.*, page 205, column 2, emphasis added).

Claims 1, 10 and 11 have been amended to recite methods comprising a) crosslinking DNA binding protein to genomic DNA of the cell; b) generating DNA fragments of the genomic DNA crosslinked to DNA binding protein; c) removing a DNA fragment to which the protein of interest is bound; d) separating the DNA fragment from the protein of interest; e) amplifying the DNA fragment; and f) combining the DNA fragment with ***a DNA microarray*** comprising one or more sequences complementary to one or more intergenic regions of genomic DNA of the cell under conditions in which hybridization occurs.

Orlando *et al.* do not anticipate the subject matter of Claims 1, 10, 11 and claims which depend therefrom, particularly as amended. In addition, Orlando *et al.* do not anticipate the subject matter of new Claims 71-86 which is directed to a method of identifying regions across a genome of a cell where binding of DNA binding proteins occurs.

Rejection of Claims 1-11, 15-22, 25-36, 39-53 and 56-68 under 35 U.S.C. §102(e)

Claims 1-11, 15-22, 25-36, 39-53 and 56-68 are rejected under 35 U.S.C. §102(e) "as being anticipated by Mercola (U.S. Patent 6,410,233)" (Office Action, page 5). Referring to Figure 1 of Mercola *et al.*, the Examiner states that Mercola *et al.* teach "a method of claims 1, 9, 10 and 11 for identifying a region of a genome of a cell to which a protein of interest binds" comprising the step of combining an amplified DNA fragment with "DNA comprising sequences complementary to intergenic regions of genomic DNA of the cell" (Office Action, pages 5-6).

Applicants respectfully disagree. Applicants' claimed invention is directed to a method of identifying a region of a genome of a cell to which a protein of interest binds comprising, *inter alia*, combining a DNA fragment to which a protein of interest binds with a DNA microarray, wherein the DNA microarray comprises one or more sequences complementary to one or more ***intergenic regions*** of genomic DNA under conditions in which hybridization occurs, and identifying the ***intergenic region*** to which the DNA fragment hybridizes.

Mercola *et al.* teach "methods for the identification of ***nucleic acid molecules corresponding to genes*** regulated by a transcription factor" (Mercola *et al.*, abstract, emphasis added). In Figure 1, Mercola *et al.* clearly show use of the DNA fragments isolated according to

the invention, to "probe ***cDNA arrays*** on a matrix" (Mercola *et al.*, Figure 1, emphasis added). cDNAs are copies of copies of gene sequences, and therefore, are not intergenic sequences even though they might include non-coding regions such as 5' or 3' untranslated regions.

In summarizing the invention, Mercola *et al.* teach that in "one aspect" the invention is "a method for isolating at least one nucleic acid molecule ***comprising at least a portion of a gene***" (Mercola *et al.*, column 2, lines 50-52 and column 10, lines 40-41, emphasis added). In this embodiment, Mercola *et al.* teach crosslinking at least one transcription factor to a nucleic acid molecule in at least one cell or nucleus to form a transcription factor/nucleic acid molecule complex (Mercola *et al.*, column 2, lines 52-55 and column 11, lines 31-56); fragmenting the nucleic acid molecule to form a transcription factor/nucleic acid molecule fragment (Mercola *et al.*, column 2, lines 55-57 and column 12, lines 11-21); isolating the nucleic acid molecule fragment from the transcription factor/nucleic acid molecule fragment, wherein the isolated nucleic acid fragment "comprises at least ***a portion of the first exon of a gene***" (Mercola *et al.*, column 2, lines 57-62 and column 10, lines 52-55, emphasis added, and column 12, lines 38-47). Mercola further teach that the nucleic acid molecule fragment can be amplified (Mercola *et al.*, column 12, line 48 - column 13, line 41). Mercola *et al.* state that such sequences of the nucleic acid molecule fragments "can be compared to databases of sequences such as they are known in the art or later developed to identify ***novel genes***" (Mercola *et al.*, column 3, lines 5-8, emphasis added, and column 13, lines 65-67). Mercola *et al.* note that the nucleic acid molecule fragments can be linked to a detectable label and "used to screen arrays of nucleic acids such as those including ***cDNA libraries*** (Mercola *et al.*, column 15, lines 1-5, emphasis added).

In the other aspect of the invention, Mercola *et al.* teach a method for isolating a nucleic acid molecule that includes at least a portion of a gene using a cDNA molecule (Mercola *et al.*, column 3, lines 13-50 and column 15, lines 9-11). Specifically, Mercola *et al.* teach crosslinking at least one transcription factor to a nucleic acid molecule in at least one cell or nucleus to form a transcription factor/nucleic acid molecule complex (Mercola *et al.*, column 3, lines 17-20 and column15, lines 15-18); fragmenting the nucleic acid molecule to form a transcription factor/nucleic acid molecule fragment (Mercola *et al.*, column 3, lines 20-22 and column 15, lines 18-20); isolating the nucleic acid molecule fragment from the transcription factor/nucleic acid molecule fragment (column 3, lines 22-24 and column 15, lines 20-22); and combining the

isolated nucleic acid molecule fragment with either "a ***cDNA library, or cDNA derived from reverse transcription of a population of RNA molecules***, to form a mixture comprising isolated nucleic acid molecule fragments/cDNA complexes (Mercola *et al.*, column 3, lines 26-28 and column 15, lines 24-27, emphasis added); and isolating the cDNA that binds with the isolated nucleic acid molecule fragment" (Mercola *et al.*, column 3, lines 30-31 and column 15, lines 29-31).

Clearly, Mercola *et al.* do not teach a method of identifying a region of a genome of a cell to which a protein of interest binds comprising, *inter alia*, combining a DNA fragment to which a protein of interest binds with a DNA microarray, wherein the DNA microarray comprises one or more sequences complementary to one or more ***intergenic regions*** of genomic DNA under conditions in which hybridization occurs, and identifying the ***intergenic region*** to which the DNA fragment hybridizes.

Mercola *et al.* do not anticipate the subject matter of Applicants' claimed invention.

Rejection of Claims 9, 15, 16, 25-36, 46, 47, 62 and 63 under 35 U.S.C. §103(a)

Claims 9, 15, 16, 25-36, 46, 47, 62 and 63 are rejected under 35 U.S.C. §103(a) as being unpatentable over Orlando *et al.* in view of Hacia *et al.* (Office Action, page 6). However, on pages 9 and 10 of the Office Action, the Examiner discusses the rejection with regard to Claims 2, 3, 4, 5, 6, 39, 40, 41, 42, 43, 56, 57, 58, 59 (Office Action, page 9) and Claims 7, 8, 17, 18-22, 44, 45, 48, 49-53, 60, 61, 64 and 65-68 (Office Action, pag 10). Clarification of the claims rejected on this basis is respectfully requested.

Specifically, the Examiner states that Orlando *et al.* teach Applicants' invention, however, Orlando *et al.* do not "teach the use of fluorescent labels, and in particular the use of Cy5" (Office Action, page 10). The Examiner states that Hacia *et al.* teach "the use of a two label system where one of the labels is Cy5-phycoerythrin" (Office Action, page 10). It is the Examiner's opinion that:

> It would have been prima facie obvious to one of ordinary skill in the art at the time the invention was made to substitute the fluorescent Cy5 dye of Hacia into the detection method of Orlando since the use of fluorescent dye permits replacement of the radioactive components used in Orlando and avoidance of radioactivity is desired . . . So an ordinary practitioner, wishing to modify

> Orlando in order to solve Orlando's concern regarding background and specificity . . . would have been motivated to use the two color system of Hacia since the two color system would improve signal specificity and accuracy as taught by Hacia . . . Further motivation to use Cy5 is that minimal spectral overlap is imposed when this dye is used in combination with phycoerythrin as discussed by Hacia (Office Action, pages 10-11).

Applicants respectfully disagree. Where the claimed invention is rejected as obvious in view of a combination of references, § 103 requires both (1) that "the prior art would have suggested to the person of ordinary skill in the art that they should . . . carry out the claimed process"; and (2) that the prior art should establish a reasonable expectation of success (*In re Vaeck*, 20 USPQ2d 1438, 1442 (Fed. Cir. 1991)). "Both the suggestion and the reasonable expectation of success must be founded in the prior art, not in the applicant's disclosure." *Id.* There is no particular teaching in the art cited directing the skilled person to identify a region of a genome of a cell to which a protein of interest binds using a DNA microarray as claimed in Applicants' method.

As pointed out above, Orlando *et al.* teach "a PCR and hybridization strategy that allows the identification of all binding sites of ***a particular protein*** within a genomic region of interest. DNA associated with specifically immunopurified chromatin is amplified by PCR and used ***as a probe in a Southern analysis*** of ***a given genomic region***" (Orlando *et al.*, page 205, column 2, emphasis added). The Examiner states that the southern blot of Orlando *et al.* "is a type of microarray" (Office Action, page 10). Therefore, it appears as if the Examiner is asserting that the Southern analysis of Orlando *et al.* is equivalent to the DNA microarray of Applicants' claimed invention.

Applicants respectfully disagree. Orlando *et al.* clearly teach that a "major difficulty is presented in the discrimination of background versus real signal in the Southern analysis" (Orlando *et al.*, page 214, column 1). Specifically, Orlando *et al.* teach that:

> For regions where the enrichment is large (for example in Polycomb immunoprecipitations), this background becomes negligible; however, the signal-to-background ratio may become significant in cases where a particular sequence is only weakly enriched during the immunoprecipitation. For example, if genomic DNA is hybridized for long periods to the genomic walk, a uniform hybridization of all bands may be seen (Orlando *et al.*, page 213, column 1).

In contrast, Applicants teach that "the present invention provides a method for non-specifically amplifying DNA fragments from the entire genome of a cell . . . which can be used without increasing the signal-to noise-ratio" (specification, page 15, lines 9-12). Applicants further teach that:

> Using the methods of the present invention also provides for the ability to compare the sample with the control sample simultaneously. Generally, a test sample if [sic] hybridized to an array and compared to a control sample which has been hybridized to a different array and a ratios [sic] is calculated to determine binding results. Using the methods described herein, two samples (*e.g.*, a test sample and a control sample) can be hybridized to the same array which allows for elimination of noise due to the use of two arrays (*e.g.*, an array for the test sample and another array for the control sample). The difference between arrays due to manufacturing artifacts is a major source of noise, which can be eliminated using the methods described herein (specification, page 16, lines 12-20).

Clearly, the Southern analysis of Orlando *et al.* is not equivalent to the microarray analysis of Applicants' claimed invention.

Orlando *et al.* state that a "number of solutions to this problem can be suggested" (Orlando *et al.*, page 213, column 1), none of which involve the use of DNA microarrays. For example, Orlando *et al.* teach that:

> if sequences are known that do not interact with the protein of interest, then the amount of hybridization to these sequences can set the background level. Alternatively the signal generated from hybridizing DNA from control immunoprecipitations (labeled to the same specific activity) can be quantified and subtracted from the values of the actual immunoprecipitation (Orlando *et al.*, page 213, column 1).

Orlando *et al.* further note that "repetitive elements will always hybridize strongly . . . In these cases the signal resulting from specific immunoprecipitation cannot be accurately determined" (Orlando *et al.*, page 213, columns 1-2).

It is the Examiner's opinion that "motivation to use the Cy5 dye of Hacia is provided by Hacia, who notes 'An attractive aspect of this two color system is the minimal spectral overlap between the phycoerythrin and phycoerythrin-Cy5 dyes . . .'" and that "'Two color analysis allows competitive hybridization between a reference standard and an unknown sample, improving the performance of the assay'" (Office Action, pages 10-11).

However, "the assay" that Hacia *et al.* refer to is a "mutational analysis of the 3.43 kb exon 11 of the hereditary breast and ovarian cancer gene *BRAC1*"(Hacia *et al.*, abstract). Hacia *et al.* note that "[h]igh density oligonucleotide arrays (DNA chips) have been used in two color mutational analysis" and that "[t]wo color analysis allows competitive hybridization between a reference standard and an unknown sample, improving the performance" of (Hacia *et al.*, abstract). Hacia *et al.* teach that replacing "a phycoerythrin-streptavidin conjugate which produces fluorescein (green) and phycoerythrin (red) hybridization signals" with a "two color red (phycoerythrin) and far-red (phycoerythrin•cy5) dye system" provides "more evenly matched signal intensities and deceased spectral overlap between the two fluorophores" in the assay (Hacia *et al.*, page 3865, abstract, column 2). Hacia *et al.* do not teach or suggest use of the two dye system in a method to identify a region of a genome of a cell to which a protein of interest binds or to non-specifically amplify DNA fragments from the entire genome of a cell. The Hacia *et al.* reference is directed to the mutational analysis of a single gene (*BRAC1* gene).

In discussing obviousness, the court has stated that:

> [a]n invention is not obvious merely because it is a combination of old elements each of which was well known in the art at the time the invention was made. . . Rather, if such a combination is novel, the issue is whether bringing them together as taught by the patentee was obvious in light of the prior art. . . The critical inquiry is whether 'there is something in the prior art as a whole to *suggest* the desirability, and thus obviousness of making the invention' (*Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*13 USPQ2d 1737 at 1765).

That is, the issue is "whether the teachings of the prior art would, *in and of themselves and without the benefit of appellant's disclosure,* make the invention as a whole, obvious" (*In re Sponnoble* 160 USPQ237 at 243 (CCPA 1969)).

There is nothing in the combined teaching of Orlando *et al.* and Hacia *et al.* that directs one of skill in the art to identify a region of a genome of a cell to which a protein of interest binds using a DNA microarray as claimed in Applicants' method. The prior art combination of record has been made with the advantage of impermissible hindsight, and thus, the rejection is legally improper. That is, in making the obviousness rejection, the Examiner has read the prior art with the benefit of Applicants' disclosure in which there is a clear teaching of the desirability of using a DNA microarray to identify a region of a genome of a cell to which a protein of interest binds.

As the court made clear in *In re Dow*, it is not legally correct to rely on Applicants' disclosure for the suggestion that the cited references should be combined and the expectation of success (*In re Dow Chemical*, 5 U.S.P.Q.2d 1529, 1531-1532 (Fed. Cir. 1988)). In the present case, the suggestion or motivation for combining the references and the expectation of success are not found in the prior art, but rather in Applicant's disclosure.

The combined teaching of the Orlando *et al.* and Hacia *et al.* references do not render obvious Applicants' claimed invention.

Rejection of Claims 23, 24, 37, 38, 54, 55, 69 and 70 under 35 U.S.C. §103(a)

Claims 23, 24, 37, 38, 54, 55, 69 and 70 are rejected under 35 U.S.C. §103(a) as being unpatentable over Orlando *et al.* in view of Hacia *et al.* and further in view of Hallahan *et al.* (Office Action, page 11). The Examiner refers to the discussion of Orlando *et al.* and Hacia *et al.* provided above and further states that "Orlando clearly teaches that the method of analysis is generic, noting 'We have substantially broadened the potential of the method by adapting it to the analysis of general transcription factors'" (Office Action, page 11). The Examiner notes however, that "Orlando in view of Hacia do not teach the species of cell cycle transcription factors" (Office Action, page 11). The Examiner cites Hallahan *et al.* as teaching "the analysis of transcription factors that are associated with cell cycle and in particular, analyzed the G1, S and G2/M transitions" (Office Action, page 12). It is the Examiner's opinion that:

> An ordinary practitioner would have been motivated to use the method of Orlando to study the transcription factors of Hallahan in order to determine where the transcription factors bind on the genomic DNA, in order to determine the higher order structure which controls gene transcription of these cell cycle factors of Hallahan (Office Action, page 12).

Applicants respectfully disagree. As indicated above, there is nothing in the combined teaching of Orlando *et al.* and Hacia *et al.* that directs one of skill in the art to identify a region of a genome of a cell to which a protein of interest binds or to non-specifically amplify DNA fragments from the entire genome of a cell, using a DNA microarray as claimed in Applicants' method. Hallahan *et al.* do not cure the deficiencies of the Orlando *et al.* and Hacia *et al.* references.

Hallahan *et al.* studied the role of the immediate early genes, *c-jun* and *Egr-1* "in cell cycle kinetics and cell survival following x-ray irradiation of clones containing inducible dominant negatives to *c-jun* and *Egr-1*" (Hallahan *et al.*, abstract). Hallahan *et al.* show that "the dominant negatives to the stress-inducible immediate early genes *Egr-1* and *c-jun* prevent the onset of S phase and reduce the survival of human cells exposed to ionizing radiation" (Hallahan *et al.*, abstract).

The combined teaching of the Orlando *et al.*, Hacia *et al.* and Hallahan *et al.* references do not render obvious Applicants' claimed invention.

Rejection of claims 23, 24, 37, 38, 54, 55, 69 and 70 under 35 U.S.C. §103(a)

Claims 23, 24, 37, 38, 54, 55, 69 and 70 are rejected under 35 U.S.C. §103(a) as being unpatentable over Mercola in view of Hallahan *et al.* (Office Action, page 12). The Examiner refers to the discussion of Mercola *et al.* above, but notes that Mercola *et al.* do not teach "the species of cell cycle transcription factors" (Office Action, page 12). The Examiner cites Hallahan *et al.* as teaching "the analysis of transcription factors that are associated with cell cycle and in particular, analyzed the G1, S and G2/M transitions" (Office Action, page 12). It is the Examiner's opinion that:

> It would have been prima facie obvious to one of ordinary skill in the art at the time the invention was made to apply the method of Mercola to any transcription factor, including cell cycle transcription factors such as those of Hallahan since an ordinary practitioner would have been motivated to use the method of Mercola to study the transcription factors of Hallahan in order to determine where the transcription factors bind on the genomic DNA, in order to determine the higher order structure which controls gene transcription of these cell cycle factors of Hallahan (Office Action, page 13).

Applicants respectfully disagree. As discussed above, Mercola *et al.* do not teach a method of identifying a region of a genome of a cell to which a protein of interest binds comprising, *inter alia*, combining a DNA fragment to which a protein of interest binds with a DNA microarray, wherein the DNA microarray comprises one or more sequences complementary to one or more ***intergenic regions*** of genomic DNA under conditions in which

hybridization occurs, and identifying the ***intergenic region*** to which the DNA fragment hybridizes. Hallahan *et al.* do not cure the deficiency of the Mercola *et al.* reference.

As discussed above, Hallahan *et al.* show that "the dominant negatives to the stress-inducible immediate early genes *Egr-1* and *c-jun* prevent the onset of S phase and reduce the survival of human cells exposed to ionizing radiation" (Hallahan *et al.*, abstract).

The combined teaching of the Mercola *et al.* and Hallahan *et al.* references do not render obvious Applicants' claimed invention.

Rejection of Claims 1-11 and 15-70 under the judicially created doctrine of obviousness-type double patenting

Claims 1-11 and 15-70 "are rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claims 1-11 of U.S. Patent No. 6,410,243 in view of Hacia and further in view of Hallahan" (Office Action, page 13).

Due to the provisional nature of the rejection, Applicants will address the rejection when this is the only remaining rejection in the subject application.

CONCLUSION

In view of the above amendments and remarks, it is believed that all claims are in condition for allowance, and it is respectfully requested that the application be passed to issue. If the Examiner feels that a telephone conference would expedite prosecution of this case, the Examiner is invited to call the undersigned.

Respectfully submitted,
HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

By Anne J. Collins

Anne J. Collins, Registration No. 40,564
On behalf of Dianne Rees, Registration No. 45,281
Telephone: (650) 485-5999
Facsimile: (650) 485-5487

Date: September 14, 2005